

the production of fertile pollen.

Sequence 5620 BP; 1498 A; 1360 C; 1328 G; 1430 T; 4 other;

Query Match 93.7%; Score 320.4; DB 13; Length 5620;

Best Local Similarity 98.0%; Pred. No. 5.2e-102; Matches 333; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

will-type

1 atgttaccggtttatcaacacgtttgacgggttgcggatattcttcagacatacataa 60  
1138 ATGGACCGGTTA-TCACACGTTTGACGGGGTTCGGATTATCTTCACACATATCATATA 1080  
61 gctaccggtatattcaacacgtttgacgggttgcggatattcttcagacatacataa 120  
1079 GCTACCGGTTA-TCACACGTTTGACGGGGTTCGGATTATCTTCACACATATCATATA 1020  
121 aggttaccggtttatcaacacgtttgacgggttgcggatattcttcagacatacataa 180  
1019 AGGGACCTTCGACGCTGCTCGGGGGAACATCGCGGACATCTTCTCAACACAG 960  
181 ggaagggcaaacctccggggaaggggagacatggtgagggagatattacataac 240  
955 GGAAGGCAAACTCCCGGCAAAAGCGACGACATGCGCGGACATCTTCTCAACACAG 900  
241 atcaggttcaagaattcagacgttcttcttcttcttcttcttcttcttcttcttctt 300  
899 ATCAGGCTTCGACGCTGCTCGGGGGAACATCGCGGACATCTTCTCAACACAG 840  
301 aacgagcattatcagacgttcttcttcttcttcttcttcttcttcttcttcttctt 342  
839 AACGACCATATCAGCCTTTCACAAATCATGATTAACGAAA 798

RESULT 14

AAV60972 standard; DNA; 344 BP.

AAV60972;

03-DEC-1998 (first entry)

Barnase coding sequence.

Barnase: barstar; IPCR; Inverse polymerase chain reaction; phenotype: transgenic plant; hybrid seed; male sterile plant; active enzyme; regulatory protein; embryoleth seed; herbicide resistance; ss.

Synthetic.

Location/Qualifiers

Key 9.344

CDs //tag- a

product- "barnase"

MO9837211-AI.

27-AUG-1998.

20-FEB-1998; 98MC-GB00542.

21-FEB-1997; 97GB-0003681.

(GENE-) GENE SHEARS PTY LTD.

Betzner AS, Hultner E, Paul W, Perez P;

WPI; 1998-467572/40.

P-PSDB; AAW71703.

Production of transgenic plants having a desired phenotype - by

using a pair of parent plants which each produce a polypeptide which

complement each other when crossed

Example 1; Fig 1A; 58pp; English.

The present invention describes a pair of parent plants for producing seeds comprising: (a) a first parent plant containing at least 1 gene sequence encoding a polypeptide or protein A, and (b) a second parent plant containing at least 1 gene sequence encoding a polypeptide or protein B, where the polypeptides A and B, when expressed in separate plants, do not form an active enzyme, a regulatory protein or protein which affects the functionality and/or viability and/or the structural integrity of a cell, but when expressed in the same plant do form an active enzyme, regulatory protein, or protein which affects the structural integrity of a cell. Also described is a method for producing a plant having a desired phenotype by virtue of an active enzyme, a regulatory protein or a protein which affects the structural integrity of a cell comprising crossing a first line with a second line where the first line contains one or more gene sequences encoding a polypeptide or protein A but which line does not have the desired phenotype and where the second line contains one or more gene sequences encoding a polypeptide or protein B which is complementary to the polypeptide or protein A but which line does not have the desired phenotype. The method can be used for producing plants having altered phenotypes, e.g. male sterility, embryoleth seeds, altered biochemical (e.g. fatty acid) composition or herbicide resistance. The present sequence encodes barnase which is used in an example from the present invention.

Sequence 344 BP; 114 A; 80 C; 78 G; 72 T; 0 other;

Query Match

Best Local Similarity 93.5%; Score 319.6; DB 19; Length 344; Matches 322; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

8 cgttattcaacacgtttgacgggttgcggatattcttcagacatacataaactct 67  
15 caggtattcaacacgtttgacgggttgcggatattcttcagacatacataaactct 74  
68 gataattcaacacgtttgacgggttgcggatattcttcagacatacataaactct 127  
75 gataattcaacacgtttgacgggttgcggatattcttcagacatacataaactct 134  
128 cttagacgttgcgtccggggaaggggagacatcttctcaaaagggaaggg 187  
135 cttagacgttgcgtccggggaaggggagacatcttctcaaaagggaaggg 194  
188 aaactccgggcaaaagcgagacatggtgagggatattacatacataaactct 247  
195 aaactccgggcaaaagcgagacatggtgagggatattacatacataaactct 254  
248 ttcaagaattcagacgttcttcttcttcttcttcttcttcttcttcttcttctt 307  
255 ttcaagaattcagacgttcttcttcttcttcttcttcttcttcttcttcttctt 314  
308 cattatcagacattcaaaatcag 333  
315 cattatcagacattcaaaatcag 340

RESULT 15

AAQ27104 standard; DNA; 791 BP.

AAQ27104;

26-JAN-1993 (first entry)

BN ribonuclease.

Barnase; calcium; Tyl; M13; pCN1330; BN ORF; retrotransposon;

replication; ss.

Bacillus amyloliquefaciens.

inverted  
will-type

Db 2565 GCTACCTGATTAATTCATTCATCAAAATCAAGCAAGCCCTGGCTGGGAGCATCAAA 2506  
 QY 121 agggaaacttgacagcgcgcctccgggaaagacatcgcgagacatctctcaacag 180  
 Db 2505 AGGGAACCTTGCAACACCTCCTCCGGGAAAGCAGCATGCGCGAGCATCTCTCAACAG 2446  
 QY 181 ggaaggaacactccgggcaaaagcgagacacacatgctgtaagcgagatataac 240  
 Db 2445 GGAAGCAAACTCCCGGCAAAAGCGAACAATGCGGTGAAGCGGATATTATCATAC 2386  
 QY 241 atcagcttcagaaatcagacgggattcttactcaagcgactcgatcttaacaaac 300  
 Db 2385 ATCAGGCTTCAGAAATTCACACCGGATCTTACTCAAGGACTGGCTGATTTCAAAAC 2326  
 QY 301 aacggacattatcagaccttcaaaaataag 333  
 Db 2325 AACGACATTATTCAGACCTTACAAAATCAG 2293  
 IS-08-894-440-4/C  
 Sequence 7 Application US/08894440  
 Patent No. 6035346  
 Applicant: PLANT GENETIC SYSTEMS N.V.  
 Title of Invention: Method to obtain male sterile plants  
 File Reference: NMSCOR  
 Current Application Number: US/08/894,440  
 Current Filing Date: 1997-11-12  
 Number of Seq ID Nos: 4  
 Software: Patent In Ver. 2.0  
 Seq ID No 4  
 Length: 5864  
 Type: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: T-DNA of  
 OTHER INFORMATION: plasmid pPCO13  
 NAME/KEY: misc.feature  
 LOCATION: Complement((1)..(25))  
 OTHER INFORMATION: Right border of Agrobacterium T-DNA (RB)  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: Complement((98)..(330))  
 OTHER INFORMATION: region containing polyadenylation signal of gene 7  
 OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: Complement((331)..(882))  
 OTHER INFORMATION: region coding for phosphinothricin acetyl  
 OTHER INFORMATION: transferase (bar)  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: Complement((883)..(2608))  
 OTHER INFORMATION: promoter of small subunit gene of Rubisco of  
 OTHER INFORMATION: Arabidopsis (Pasu)  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: Complement((2659)..(3031))  
 OTHER INFORMATION: region containing polyadenylation signal of  
 OTHER INFORMATION: napaline synthase gene of Agrobacterium T-DNA  
 OTHER INFORMATION: (3 nos)  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: Complement((3032)..(3367))  
 OTHER INFORMATION: region coding for barnase of Bacillus  
 OTHER INFORMATION: amyloliquefaciens  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: Complement((3368)..(4877))  
 OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana

*Handwritten signature/initials*

OTHER INFORMATION: tabacum (PTA29)  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: (4924)..(5216)  
 OTHER INFORMATION: promoter of napaline synthase gene of  
 OTHER INFORMATION: Agrobacterium T-DNA (Pnos)  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: (5217)..(5489)  
 OTHER INFORMATION: region coding for barnase of Bacillus  
 OTHER INFORMATION: amyloliquefaciens  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: (5490)..(5765)  
 OTHER INFORMATION: region containing polyadenylation signal of gene 7  
 OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: Complement((5840)..(5864))  
 OTHER INFORMATION: Left border of Agrobacterium T-DNA  
 US-08-894-440-4

Query Match 93.7%; Score 320.4; DB 3; Length 5864;  
 Best Local Similarity 98.0%; Pred. No. 7.5e-102;  
 Matches 335; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 atggacgggttatcaaacagttgacggggttcgggattatcttcaagacatatacaaa 60  
 Db 3367 ATGGACGGGTTA-TCAACAGTTTGACGGGCTTGCGGATTTCAAGCATATCATTA 3309  
 QY 61 gctaccggaattacattacaataatcagaagcagcctcgctgggtggatcaaa 120  
 Db 3308 GCTACCGGATTAATTACATTACAAATCAGAGCACAAGCCTTCGCTGGGTGGCATCAAA 3249  
 QY 121 agggaaacttgacagcgcgcctccgggaaagacatcgcgagacatcttcaaacag 180  
 Db 3248 AGGGAACCTTGCAACACCTCCTCCGGGAAAGCAGCATGCGGAGCATCTCTCAAAAG 3189  
 QY 181 ggaaggaacactccgggcaaaagcgagacatcgctgtaagcgagatataac 240  
 Db 3188 GGAAGGAACACTCCCGGCAAAAGCGAGCAGCATGCGGTCAACCGGATTTACTATAC 3129  
 QY 241 atcaggttcagaatcagacccggttcttcaacgaagcgactgctgattacaacac 300  
 Db 3128 ATCAGGCTTCAGAAATTCAGACCGGATCTTTACCAAGCAGCTGCTGATTTACAAAC 3069  
 QY 301 aacggacattatcagaccttcaaaaataagtaactaga 342  
 Db 3068 AACGACATTATTCAGACCTTACAAAATCAGATACGAAA 3027

Search completed: September 7, 2001, 14:47:02  
 Job time: 48 sec  
*deleted in QY*